

SEQUENCE LISTING

<110> LEWIN, DAVID
STEWART, TIMOTHY P.

<120> GENES ASSOCIATED WITH OBESITY AND METHODS
FOR USING THE SAME

<130> 09800081-0047C

<150> 09/691,439

<151> 2000-10-18

<150> 60/160,246

<151> 1999-10-19

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 1238

<212> DNA

<213> Mus sp.

<400> 1

```

ttatcttggc ttggatttga ttttctgtat cagtaactga ccatagtgtt aaagtattaa 60
aatggagacc cagacccaaa gcataaaaaag gcacacagtc atggtctttc tcctacgtga 120
ccttagcttt gcatgatttg aaaacaaaaa agttttttta aaaaagattt atttatttat 180
tatatgtgat ataaactact ttaaatagat ttgtatatta aagaaaacca aaacaaactc 240
aaccaatcca tggcagccaa aattttatat aactagggac tctccaatgg gaagaggcca 300
aataaacagc tgtggagctg taaccaatca cgttggcttg gcgtttatgc ctccctaata 360
agttagtcc cacctgaagt gcctgggcca cacaggggtt ggagctgcc agcaacaact 420
ggtgtttgct cagatacact gtaacccttt aagggtgcctc agctgacact ttaacgttaa 480
gcagttacct aatgtagtac aggtatcata atctaagtct tgaagctcat gaggtttata 540
acgctgttat tctcacgaaa gtcacgtgac atagctttct ataacatgct atagtagtcc 600
ccgtacctcc aagtgttgct tttttagaga gaatgatttc cagggtcatt gaggtcactg 660
aggtaaggag gccccagggtg aatgaccac agtgctccttg taaaaagaga cacacacaga 720
ggggcgatga aatgcagaca ctgaatgaag atgaccaacc atcttccatc tcaggaagga 780
ccaaacactt cggaagctg tgagaagcct attttagagc tctagagaag atctacacac 840
acacacacac acacacacac acacacacac acacacacac acgacatctg gctgccagca 900
gtgtgagaca gacagacatt tctgttgttt tgagccactt agttgtagta ttttgtaga 960
gcatccctag gaagctagag cgctcctctt actctacacc ggtacatct caggagtccc 1020
ccatggatgg atggtggaag ctgcagacta tcagcccctg tgtgtcctgt ttttctgtat 1080
tcatttatgc ttatgataaa gtgtaacttg taaattaggc aaaggaagaa ataaacaact 1140
actaatagta aataactcac attagaatga ttataatata ctgtgtaact ttgtaagcaa 1200
tatactgcaa taaatgtttt gcgactgggc cctccctt 1238

```

<210> 2

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 2
 atgtatcaca gcctgtacct g 21

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 3
 ttcttgggtct cttcctcctt g 21

<210> 4
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe

<400> 4
 aggtctaaga ccaaggaagc acgcaa 26

<210> 5
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 agcaaccgcg ccaagg 16

<210> 6
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 gcgtctggct cttctcgg 18

<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 7
caagcgttac ggtggcttca tgacc 25

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
cagaccagcg aataacaagc g 21

<210> 9
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gaagccgagg tgcctgtgt 19

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 10
tgacctgcac aatgactgca cagagacc 28

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
cctgctgttc tgccaaaatg t 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

 <400> 12
 tcggagagaa gtctggcagt c 21

 <210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe

 <400> 13
 agcctctgcc aatctgttcc gctg 24

 <210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 14
 ttgttttgtg gaccaccgaa 20

 <210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 15
 tcaaagccga ggcattgttt 20

 <210> 16
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe

 <400> 16
 caaccgatga ctcttttctc tcacctgct 29

 <210> 17
 <211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 17
 aactctgggt cccttgaaga aaatatt 27

 <210> 18
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 18
 gtgagtatgc ctaccaaagt ttgtg 25

 <210> 19
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe

 <400> 19
 aggtgtggtg acgcctgcct ctttaa 26

 <210> 20
 <211> 1237
 <212> DNA
 <213> Mus sp.

 <220>
 <221> CDS
 <222> (1)..(1236)

 <400> 20
 aag gga ggg ccc agt cgc aaa aca ttt att gca gta tat tgc tta caa 48
 Lys Gly Gly Pro Ser Arg Lys Thr Phe Ile Ala Val Tyr Cys Leu Gln
 1 5 10 15

 agt tac aca gta tat tat aat cat tct aat gtg agt tat tta cta tta 96
 Ser Tyr Thr Val Tyr Tyr Asn His Ser Asn Val Ser Tyr Leu Leu Leu
 20 25 30

 gta gtt gtt tat ttc ttc ctt tgc cta att tac aag tta cac ttt atc 144
 Val Val Val Tyr Phe Phe Leu Cys Leu Ile Tyr Lys Leu His Phe Ile
 35 40 45

 ata agc ata aat gaa tac aga aaa aca gga cac aca ggg gct gat agt 192
 Ile Ser Ile Asn Glu Tyr Arg Lys Thr Gly His Thr Gly Ala Asp Ser

50	55	60	
ctg cag ctt cca cca tcc atc cat ggg gga ctc ctg aga tgt acc cgg			240
Leu Gln Leu Pro Pro Ser Ile His Gly Gly Leu Leu Arg Cys Thr Arg			
65	70	75	80
tgt aga gta aga gga gcg ctc tag ctt cct agg gat gct cta aca aaa			288
Cys Arg Val Arg Gly Ala Leu	Leu Pro Arg Asp Ala Leu Thr Lys		
85	90		95
tac tac aac taa gtg gct caa aac aac aga aat gtc tgt ctg tct cac			336
Tyr Tyr Asn	Val Ala Gln Asn Asn Arg Asn Val Cys Leu Ser His		
100	105		110
act gct ggc agc cag atg tcg tgt gtg tgt gtg tgt gtg tgt gtg			384
Thr Ala Gly Ser Gln Met Ser Cys Val Cys Val Cys Val Cys Val Cys			
115	120		125
gtg tgt gtg tgt gtg tgt gta gat ctt ctc tag agc tct aaa ata ggc			432
Val Cys Val Cys Val Cys Val Asp Leu Leu	Ser Ser Lys Ile Gly		
130	135		140
ttc tca cag ctt ccc gaa gtg ttt ggt cct tcc tga gat gga aga tgg			480
Phe Ser Gln Leu Pro Glu Val Phe Gly Pro Ser	Asp Gly Arg Trp		
145	150		155
ttg gtc atc ttc att cag tgt ctg cat ttc atc gcc cct ctg tgt gtg			528
Leu Val Ile Phe Ile Gln Cys Leu His Phe Ile Ala Pro Leu Cys Val			
160	165		170
tct ctt ttt aca agg aca ctg tgg gtc att cac ctg ggg cct cct tac			576
Ser Leu Phe Thr Arg Thr Leu Trp Val Ile His Leu Gly Pro Pro Tyr			
175	180		185
ctc agt gac ctc aat gac cct gga aat cat tct ctc taa aaa gac aac			624
Leu Ser Asp Leu Asn Asp Pro Gly Asn His Ser Leu	Lys Asp Asn		
190	195		200
act tgg agg tac ggg gac tac tat agc atg tta tag aaa gct atg tca			672
Thr Trp Arg Tyr Gly Asp Tyr Tyr Ser Met Leu	Lys Ala Met Ser		
205	210		215
cgt gac ttt cgt gag aat aac agc gtt ata aac ctc atg agc ttc aag			720
Arg Asp Phe Arg Glu Asn Asn Ser Val Ile Asn Leu Met Ser Phe Lys			
220	225		230
act tag att atg ata cct gta cta cat tag gta act gct taa cgt taa			768
Thr	Ile Met Ile Pro Val Leu His	Val Thr Ala	Arg
235	240		245
agt gtc agc tga ggc acc tta aag ggt tac agt gta tct gag caa aca			816
Ser Val Ser	Gly Thr Leu Lys Gly Tyr Ser Val Ser Glu Gln Thr		
250	255		260
cca gtt gtt gct ggg cag ctc caa ccc ctg tgt ggc cca ggc act tca			864
Pro Val Val Ala Gly Gln Leu Gln Pro Leu Cys Gly Pro Gly Thr Ser			
265	270		275

His	Thr	His	Thr	His	Thr	Thr	Ser	Gly	Cys	Gln	Gln	Cys	Glu	Thr	Asp	
270						275					280					
aga	cat	ttc	tgt	tgt	ttt	gag	cca	ctt	agt	tgt	agt	att	ttg	tta	gag	960
Arg	His	Phe	Cys	Cys	Phe	Glu	Pro	Leu	Ser	Cys	Ser	Ile	Leu	Leu	Glu	
285					290					295					300	
cat	ccc	tag	gaa	gct	aga	gcg	ctc	ctc	tta	ctc	tac	acc	ggg	tac	atc	1008
His	Pro		Glu	Ala	Arg	Ala	Leu	Leu	Leu	Leu	Tyr	Thr	Gly	Tyr	Ile	
					305					310					315	
tca	gga	gtc	ccc	cat	gga	tgg	atg	gtg	gaa	gct	gca	gac	tat	cag	ccc	1056
Ser	Gly	Val	Pro	His	Gly	Trp	Met	Val	Glu	Ala	Ala	Asp	Tyr	Gln	Pro	
				320					325					330		
ctg	tgt	gtc	ctg	ttt	ttc	tgt	att	cat	tta	tgc	tta	tga	taa	agt	gta	1104
Leu	Cys	Val	Leu	Phe	Phe	Cys	Ile	His	Leu	Cys	Leu			Ser	Val	
			335					340							345	
act	tgt	aaa	tta	ggc	aaa	gga	aga	aat	aaa	caa	cta	cta	ata	gta	aat	1152
Thr	Cys	Lys	Leu	Gly	Lys	Gly	Arg	Asn	Lys	Gln	Leu	Leu	Ile	Val	Asn	
				350					355					360		
aac	tca	cat	tag	aat	gat	tat	aat	ata	ctg	tgt	aac	ttt	gta	agc	aat	1200
Asn	Ser	His		Asn	Asp	Tyr	Asn	Ile	Leu	Cys	Asn	Phe	Val	Ser	Asn	
				365					370					375		
ata	ctg	caa	taa	atg	ttt	tgc	gac	tgg	gcc	ctc	cct	t				1237
Ile	Leu	Gln		Met	Phe	Cys	Asp	Trp	Ala	Leu	Pro					
				380					385							

<210> 22
 <211> 393
 <212> PRT
 <213> Mus sp.

<400> 22
 Lys Gly Gly Pro Ser Arg Lys Thr Phe Ile Ala Val Tyr Cys Leu Gln
 1 5 10 15
 Ser Tyr Thr Val Tyr Tyr Asn His Ser Asn Val Ser Tyr Leu Leu Leu
 20 25 30
 Val Val Val Tyr Phe Phe Leu Cys Leu Ile Tyr Lys Leu His Phe Ile
 35 40 45
 Ile Ser Ile Asn Glu Tyr Arg Lys Thr Gly His Thr Gly Ala Asp Ser
 50 55 60
 Leu Gln Leu Pro Pro Ser Ile His Gly Gly Leu Leu Arg Cys Thr Arg
 65 70 75 80
 Cys Arg Val Arg Gly Ala Leu Leu Pro Arg Asp Ala Leu Thr Lys Tyr
 85 90 95
 Tyr Asn Val Ala Gln Asn Asn Arg Asn Val Cys Leu Ser His Thr Ala
 100 105 110

Gly	Ser	Gln	Met	Ser	Cys	Val	Cys	Val	Cys	Val	Cys	Val	Cys	Val	Cys		115	120	125
Val	Cys	Val	Cys	Val	Asp	Leu	Leu	Ser	Ser	Lys	Ile	Gly	Phe	Ser	Gln		130	135	140
Leu	Pro	Glu	Val	Phe	Gly	Pro	Ser	Asp	Gly	Arg	Trp	Leu	Val	Ile	Phe		145	150	155
Ile	Gln	Cys	Leu	His	Phe	Ile	Ala	Pro	Leu	Cys	Val	Ser	Leu	Phe	Thr		165	170	175
Arg	Thr	Leu	Trp	Val	Ile	His	Leu	Gly	Pro	Pro	Tyr	Leu	Ser	Asp	Leu		180	185	190
Asn	Asp	Pro	Gly	Asn	His	Ser	Leu	Lys	Asp	Asn	Thr	Trp	Arg	Tyr	Gly		195	200	205
Asp	Tyr	Tyr	Ser	Met	Leu	Lys	Ala	Met	Ser	Arg	Asp	Phe	Arg	Glu	Asn		210	215	220
Asn	Ser	Val	Ile	Asn	Leu	Met	Ser	Phe	Lys	Thr	Ile	Met	Ile	Pro	Val		225	230	235
Leu	His	Val	Thr	Ala	Arg	Ser	Val	Ser	Gly	Thr	Leu	Lys	Gly	Tyr	Ser		245	250	255
Val	Ser	Glu	Gln	Thr	Pro	Val	Val	Ala	Gly	Gln	Leu	Gln	Pro	Leu	Cys		260	265	270
Gly	Pro	Gly	Thr	Ser	Gly	Gly	Asn	Leu	Ile	Arg	Glu	Ala	Thr	Pro	Ser		275	280	285
Gln	Arg	Asp	Trp	Leu	Gln	Leu	His	Ser	Cys	Leu	Phe	Gly	Leu	Phe	Pro		290	295	300
Leu	Glu	Ser	Pro	Leu	Tyr	Lys	Ile	Leu	Ala	Ala	Met	Asp	Trp	Leu	Ser		305	310	315
Leu	Phe	Trp	Phe	Ser	Leu	Ile	Tyr	Lys	Ser	Ile	Ser	Ser	Leu	Tyr	His		325	330	335
Ile	Ile	Asn	Lys	Ser	Phe	Leu	Lys	Lys	Leu	Phe	Cys	Phe	Gln	Ile	Met		340	345	350
Gln	Ser	Gly	His	Val	Gly	Glu	Arg	Pro	Leu	Cys	Ala	Phe	Leu	Cys	Phe		355	360	365
Gly	Ser	Gly	Leu	His	Phe	Asn	Thr	Leu	Thr	Leu	Trp	Ser	Val	Thr	Asp		370	375	380
Thr	Glu	Asn	Gln	Ile	Gln	Ala	Lys	Ile									385	390	

<210> 23
<211> 389

<212> PRT
 <213> Mus sp.

<400> 23

Arg	Glu	Gly	Pro	Val	Ala	Lys	His	Leu	Leu	Gln	Tyr	Ile	Ala	Tyr	Lys	1	5	10	15
Val	Thr	Gln	Tyr	Ile	Ile	Ile	Ile	Leu	Met	Val	Ile	Tyr	Tyr	Leu	Phe	20	25	30	
Ile	Ser	Ser	Phe	Ala	Phe	Thr	Ser	Tyr	Thr	Leu	Ser	Ala	Met	Asn	Thr	35	40	45	
Glu	Lys	Gln	Asp	Thr	Gln	Gly	Leu	Ile	Val	Cys	Ser	Phe	His	His	Pro	50	55	60	
Ser	Met	Gly	Asp	Ser	Asp	Val	Pro	Gly	Val	Glu	Glu	Glu	Arg	Ser	Ser	65	70	75	80
Phe	Leu	Gly	Met	Leu	Gln	Asn	Thr	Thr	Thr	Lys	Trp	Leu	Lys	Thr	Thr	85	90	95	
Glu	Met	Ser	Val	Cys	Leu	Thr	Leu	Leu	Ala	Ala	Arg	Cys	Arg	Val	Cys	100	105	110	
Val	Cys	Val	Cys	Val	Cys	Val	Cys	Val	Cys	Val	Cys	Val	Ile	Phe	Ser	115	120	125	
Arg	Ala	Leu	Lys	Ala	Ser	His	Ser	Phe	Pro	Lys	Cys	Leu	Val	Leu	Pro	130	135	140	
Glu	Met	Glu	Asp	Gly	Trp	Ser	Ser	Ser	Phe	Ser	Val	Cys	Ile	Ser	Ser	145	150	155	160
Pro	Leu	Cys	Val	Cys	Leu	Phe	Leu	Gln	Gly	His	Cys	Gly	Ser	Phe	Thr	165	170	175	
Trp	Gly	Leu	Leu	Thr	Ser	Val	Thr	Ser	Met	Thr	Leu	Glu	Ile	Ile	Leu	180	185	190	
Ser	Lys	Lys	Thr	Thr	Leu	Gly	Gly	Thr	Gly	Thr	Thr	Ile	Ala	Cys	Tyr	195	200	205	
Arg	Lys	Leu	Cys	His	Val	Thr	Phe	Val	Arg	Ile	Thr	Ala	Leu	Thr	Ser	210	215	220	
Ala	Ser	Arg	Leu	Arg	Leu	Tyr	Leu	Tyr	Tyr	Ile	Arg	Leu	Leu	Asn	Val	225	230	235	240
Lys	Val	Ser	Ala	Glu	Ala	Pro	Arg	Val	Thr	Val	Tyr	Leu	Ser	Lys	His	245	250	255	
Gln	Leu	Leu	Leu	Gly	Ser	Ser	Asn	Pro	Cys	Val	Ala	Gln	Ala	Leu	Gln	260	265	270	
Val	Gly	Thr	Asn	Ser	Leu	Gly	Arg	His	Lys	Arg	Gln	Ala	Asn	Val	Ile	275	280	285	

Gly Tyr Ser Ser Thr Ala Val Tyr Leu Ala Ser Ser His Trp Arg Val
 290 295 300
 Pro Ser Tyr Ile Lys Phe Trp Leu Pro Trp Ile Gly Val Cys Phe Gly
 305 310 315 320
 Phe Leu Tyr Thr Asn Leu Phe Lys Val Val Tyr Ile Thr Tyr Asn Lys
 325 330 335
 Ile Asn Leu Phe Lys Asn Phe Phe Val Phe Lys Ser Cys Lys Ala Lys
 340 345 350
 Val Thr Glu Lys Asp His Asp Cys Val Pro Phe Tyr Ala Leu Gly Leu
 355 360 365
 Val Ser Ile Leu Ile Leu His Tyr Gly Gln Leu Leu Ile Gln Lys Ile
 370 375 380
 Lys Ser Lys Pro Arg
 385

<210> 24
 <211> 389
 <212> PRT
 <213> Mus sp.

<400> 24
 Gly Arg Ala Gln Ser Gln Asn Ile Tyr Cys Ser Ile Leu Leu Thr Lys
 1 5 10 15
 Leu His Ser Ile Leu Ser Phe Cys Glu Leu Phe Thr Ile Ser Ser Cys
 20 25 30
 Leu Phe Leu Pro Leu Pro Asn Leu Gln Val Thr Leu Tyr His Lys His
 35 40 45
 Lys Ile Gln Lys Asn Arg Thr His Arg Gly Ser Ala Ala Ser Thr Ile
 50 55 60
 His Pro Trp Gly Thr Pro Glu Met Tyr Pro Val Ser Lys Arg Ser Ala
 65 70 75 80
 Leu Ala Ser Gly Cys Ser Asn Lys Ile Leu Gln Leu Ser Gly Ser Lys
 85 90 95
 Gln Gln Lys Cys Leu Ser Val Ser His Cys Trp Gln Pro Asp Val Val
 100 105 110
 Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Arg
 115 120 125
 Ser Ser Leu Glu Leu Asn Arg Leu Leu Thr Ala Ser Arg Ser Val Trp
 130 135 140
 Ser Phe Leu Arg Trp Lys Met Val Gly His Leu His Ser Val Ser Ala
 145 150 155 160

Phe His Arg Pro Ser Val Cys Val Ser Phe Tyr Lys Asp Thr Val Gly
165 170 175
His Ser Pro Gly Ala Ser Leu Pro Gln Pro Gln Pro Trp Lys Ser Phe
180 185 190
Ser Leu Lys Arg Gln His Leu Glu Val Arg Gly Leu Leu His Val Ile
195 200 205
Glu Ser Tyr Val Thr Leu Ser Glu Gln Arg Tyr Lys Pro His Glu Leu
210 215 220
Gln Asp Leu Asp Tyr Asp Thr Cys Thr Thr Leu Gly Asn Cys Leu Thr
225 230 235 240
Leu Lys Cys Gln Leu Arg His Leu Lys Gly Leu Gln Cys Ile Ala Asn
245 250 255
Thr Ser Cys Cys Trp Ala Ala Pro Thr Pro Val Trp Pro Arg His Phe
260 265 270
Arg Trp Glu Leu Thr His Gly Gly Ile Asn Ala Lys Pro Thr Leu Val
275 280 285
Thr Ala Pro Gln Leu Phe Ile Trp Pro Leu Pro Ile Gly Glu Ser Leu
290 295 300
Val Ile Asn Phe Gly Cys His Gly Leu Val Glu Phe Val Leu Val Phe
305 310 315 320
Phe Asn Ile Gln Ile Tyr Leu Lys Phe Ile Ser His Ile Ile Asn Lys
325 330 335
Ile Phe Phe Lys Lys Thr Phe Leu Phe Ser Asn His Ala Lys Leu Arg
340 345 350
Ser Arg Arg Arg Lys Thr Met Thr Val Cys Leu Phe Met Leu Trp Val
355 360 365
Trp Ser Pro Phe Tyr Phe Asn Thr Met Val Ser Tyr Tyr Arg Lys Ser
370 375 380
Asn Pro Ser Gln Asp
385

<210> 25
<211> 387
<212> PRT
<213> Mus sp.

<400> 25
Leu Ser Trp Leu Gly Phe Asp Phe Leu Tyr Gln Leu Thr Ile Val Leu
1 5 10 15
Lys Tyr Asn Gly Asp Gln Thr Gln Ser Ile Lys Arg His Thr Val Met
20 25 30

Val Phe Leu Leu Arg Asp Leu Ser Phe Ala Phe Glu Asn Lys Lys Val
35 40 45
Phe Leu Lys Lys Ile Tyr Leu Phe Ile Ile Cys Asp Ile Asn Tyr Phe
50 55 60
Lys Ile Cys Ile Leu Lys Lys Thr Lys Thr Asn Ser Thr Asn Pro Trp
65 70 75 80
Gln Pro Lys Phe Tyr Ile Thr Arg Asp Ser Pro Met Gly Arg Gly Gln
85 90 95
Ile Asn Ser Cys Gly Ala Val Thr Asn His Val Gly Leu Ala Phe Met
100 105 110
Pro Pro Val Ser Ser His Leu Lys Cys Leu Gly His Thr Gly Val Gly
115 120 125
Ala Ala Gln Gln Gln Leu Val Phe Ala Gln Ile His Cys Asn Pro Leu
130 135 140
Arg Cys Leu Ser His Phe Asn Val Lys Gln Leu Pro Asn Val Val Gln
145 150 155 160
Val Ser Ser Lys Ser Ser Ser Gly Leu Arg Cys Tyr Ser His Glu Ser
165 170 175
His Val Thr Leu Ser Ile Thr Cys Tyr Ser Ser Pro Arg Thr Ser Lys
180 185 190
Cys Cys Leu Phe Arg Glu Asn Asp Phe Gln Gly His Gly His Gly Lys
195 200 205
Glu Ala Pro Gly Glu Pro Thr Val Ser Leu Lys Glu Thr His Thr Glu
210 215 220
Gly Arg Asn Ala Asp Thr Glu Arg Pro Thr Ile Phe His Leu Arg Lys
225 230 235 240
Asp Gln Thr Leu Arg Glu Ala Val Arg Ser Leu Phe Ser Ser Arg Glu
245 250 255
Asp Leu His Thr His Thr His Thr His Thr His Thr His Thr
260 265 270
His Thr Thr Ser Gly Cys Gln Gln Cys Glu Thr Asp Arg His Phe Cys
275 280 285
Cys Phe Glu Pro Leu Ser Cys Ser Ile Leu Leu Glu His Pro Glu Ala
290 295 300
Arg Ala Leu Leu Leu Leu Tyr Thr Gly Tyr Ile Ser Gly Val Pro His
305 310 315 320
Gly Trp Met Val Glu Ala Ala Asp Tyr Gln Pro Leu Cys Val Leu Phe
325 330 335
Phe Cys Ile His Leu Cys Leu Ser Val Thr Cys Lys Leu Gly Lys Gly

340 345 350
 Arg Asn Lys Gln Leu Leu Ile Val Asn Asn Ser His Asn Asp Tyr Asn
 355 360 365
 Ile Leu Cys Asn Phe Val Ser Asn Ile Leu Gln Met Phe Cys Asp Trp
 370 375 380
 Ala Leu Pro
 385

<210> 26
 <211> 389
 <212> PRT
 <213> Mus sp.

<400> 26
 Tyr Leu Gly Leu Asp Leu Ile Phe Cys Ile Ser Asn Pro Cys Ser Ile
 1 5 10 15
 Lys Met Glu Thr Arg Pro Lys Ala Lys Gly Thr Gln Ser Trp Ser Phe
 20 25 30
 Ser Tyr Val Thr Leu Ala Leu His Asp Leu Lys Thr Lys Lys Phe Phe
 35 40 45
 Lys Arg Phe Ile Tyr Leu Leu Tyr Val Ile Thr Thr Leu Asn Arg Phe
 50 55 60
 Val Tyr Arg Lys Pro Lys Gln Thr Gln Pro Ile His Gly Ser Gln Asn
 65 70 75 80
 Phe Ile Leu Gly Thr Leu Gln Trp Glu Glu Ala Lys Thr Ala Val Glu
 85 90 95
 Leu Pro Ile Thr Leu Ala Trp Arg Leu Cys Leu Pro Asn Glu Leu Val
 100 105 110
 Pro Thr Ser Ala Trp Ala Thr Gln Gly Leu Glu Leu Pro Ser Asn Asn
 115 120 125
 Trp Cys Leu Leu Arg Tyr Thr Val Thr Leu Gly Ala Ser Ala Asp Thr
 130 135 140
 Leu Thr Leu Ser Ser Tyr Leu Met Tyr Arg Tyr His Asn Leu Ser Leu
 145 150 155 160
 Glu Ala His Glu Val Tyr Asn Ala Val Ile Leu Thr Lys Val Thr His
 165 170 175
 Ser Phe Leu His Ala Ile Val Val Pro Val Pro Pro Ser Val Val Phe
 180 185 190
 Leu Glu Arg Met Ile Ser Arg Val Ile Glu Val Thr Glu Val Arg Arg
 195 200 205

Pro Gln Val Asn Asp Pro Gln Cys Pro Cys Lys Lys Arg His Thr Gln
 210 215 220
 Arg Gly Asp Glu Met Gln Thr Leu Asn Glu Asp Asp Gln Pro Ser Ser
 225 230 235 240
 Ile Ser Gly Arg Thr Lys His Phe Gly Lys Leu Glu Ala Tyr Phe Arg
 245 250 255
 Ala Leu Glu Lys Ile Tyr Thr His Thr His Thr His Thr His
 260 265 270
 Thr His Thr His Thr Arg His Leu Ala Ala Ser Ser Val Arg Gln Thr
 275 280 285
 Asp Ile Ser Val Val Leu Ser His Leu Val Val Val Phe Cys Ser Ile
 290 295 300
 Pro Arg Lys Leu Glu Arg Ser Ser Tyr Ser Thr Pro Gly Thr Ser Gln
 305 310 315 320
 Glu Ser Pro Met Asp Gly Trp Trp Lys Leu Gln Thr Ile Ser Pro Cys
 325 330 335
 Val Ser Cys Phe Ser Val Phe Ile Tyr Ala Tyr Asp Lys Val Leu Val
 340 345 350
 Asn Ala Lys Glu Glu Ile Asn Asn Tyr Ile Thr His Ile Arg Met Ile
 355 360 365
 Ile Ile Tyr Cys Val Thr Leu Ala Ile Tyr Cys Asn Lys Cys Phe Ala
 370 375 380
 Thr Gly Pro Ser Leu
 385

<210> 27
 <211> 379
 <212> PRT
 <213> Mus sp.

<400> 27
 Ile Leu Ala Trp Ile Phe Ser Val Ser Val Thr Asp His Ser Val Lys
 1 5 10 15
 Val Leu Lys Trp Arg Pro Asp Pro Lys His Lys Lys Ala His Ser His
 20 25 30
 Gly Leu Ser Pro Thr Pro Leu Cys Met Ile Lys Gln Lys Ser Phe Phe
 35 40 45
 Lys Lys Asp Leu Phe Ile Tyr Tyr Met Tyr Lys Leu Leu Ile Asp Leu
 50 55 60
 Tyr Ile Lys Glu Asn Gln Asn Lys Leu Asn Gln Ser Met Ala Ala Lys
 65 70 75 80

Ile Leu Tyr Asn Gly Leu Ser Asn Gly Lys Arg Pro Asn Lys Gln Leu
 85 90 95
 Trp Ser Cys Asn Gln Ser Arg Trp Leu Gly Val Tyr Ala Ser Leu Met
 100 105 110
 Ser Phe Pro Pro Glu Val Pro Gly Pro His Arg Gly Trp Ser Cys Pro
 115 120 125
 Ala Thr Thr Gly Val Cys Ser Asp Thr Leu Pro Phe Lys Val Pro Gln
 130 135 140
 Leu Thr Leu Arg Ala Val Thr Cys Ser Thr Gly Ile Ile Ile Val Leu
 145 150 155 160
 Lys Leu Met Arg Phe Ile Thr Leu Leu Phe Ser Arg Lys Ser Arg Asp
 165 170 175
 Ile Ala Phe Tyr Asn Met Leu Ser Pro Tyr Leu Gln Val Leu Ser Phe
 180 185 190
 Arg Glu Phe Pro Gly Ser Leu Arg Ser Leu Arg Gly Gly Pro Arg Met
 195 200 205
 Thr His Ser Val Leu Val Lys Arg Asp Thr His Arg Gly Ala Met Lys
 210 215 220
 Cys Arg His Met Lys Met Thr Asn His Leu Pro Ser Gln Glu Gly Pro
 225 230 235 240
 Asn Thr Ser Gly Ser Cys Glu Lys Pro Ile Leu Glu Leu Arg Arg Ser
 245 250 255
 Thr His Thr His Thr His Thr His Thr His Thr His Thr His Thr His
 260 265 270
 Asp Ile Trp Leu Pro Ala Val Asp Arg Gln Thr Phe Leu Leu Phe Ala
 275 280 285
 Thr Leu Tyr Phe Val Arg Ala Ser Leu Gly Ser Ser Ala Pro Leu Thr
 290 295 300
 Leu His Arg Val His Leu Arg Ser Pro Pro Trp Met Asp Gly Gly Ser
 305 310 315 320
 Cys Arg Leu Ser Ala Pro Val Cys Pro Val Phe Leu Tyr Ser Phe Met
 325 330 335
 Leu Met Ile Lys Cys Asn Leu Ile Arg Gln Arg Lys Lys Thr Thr Thr
 340 345 350
 Asn Ser Lys Leu Thr Leu Glu Leu Tyr Thr Val Leu Cys Lys Gln Tyr
 355 360 365
 Thr Ala Ile Asn Val Leu Arg Leu Gly Pro Pro
 370 375